

Figure 1(a)

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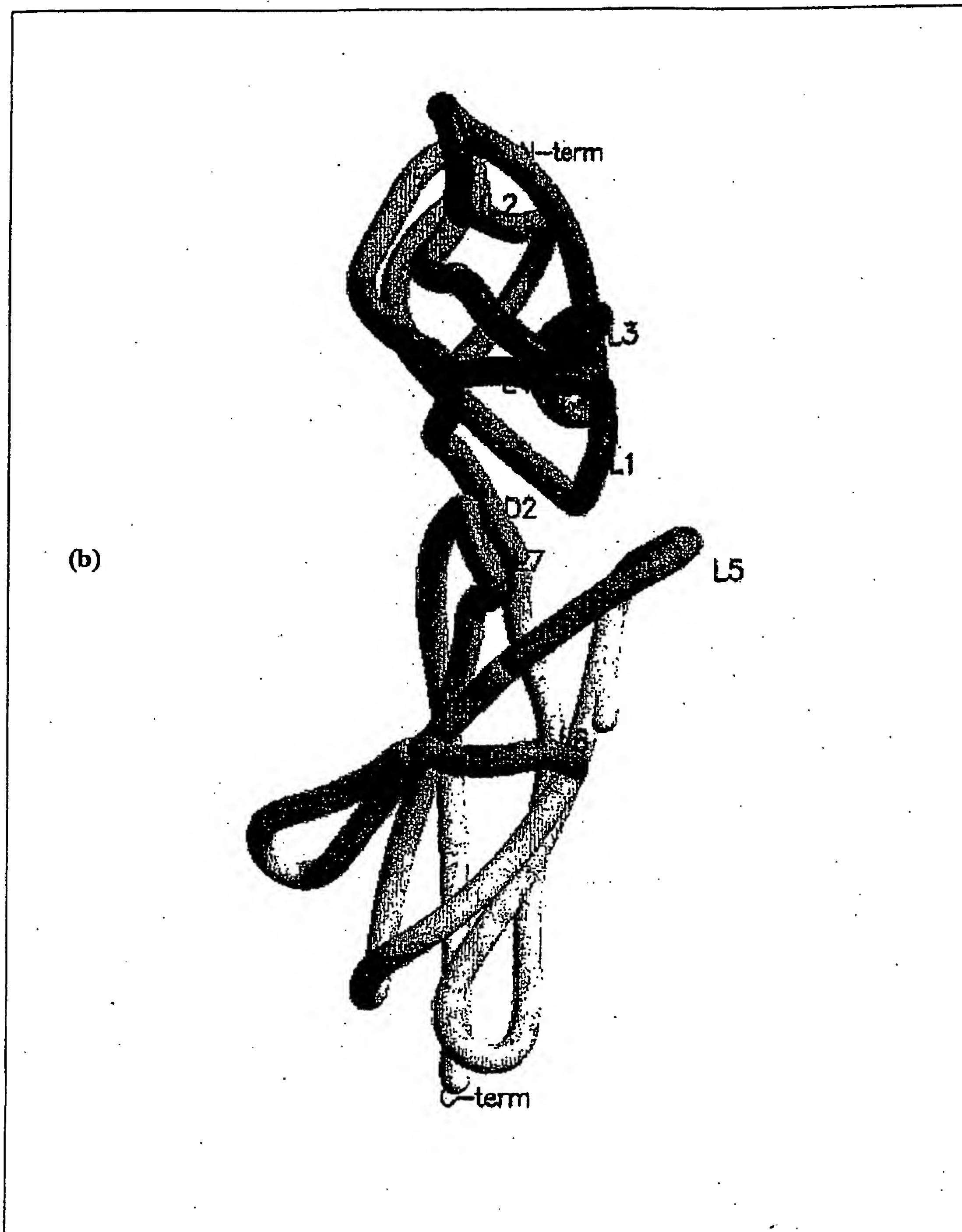


Figure 1(b)

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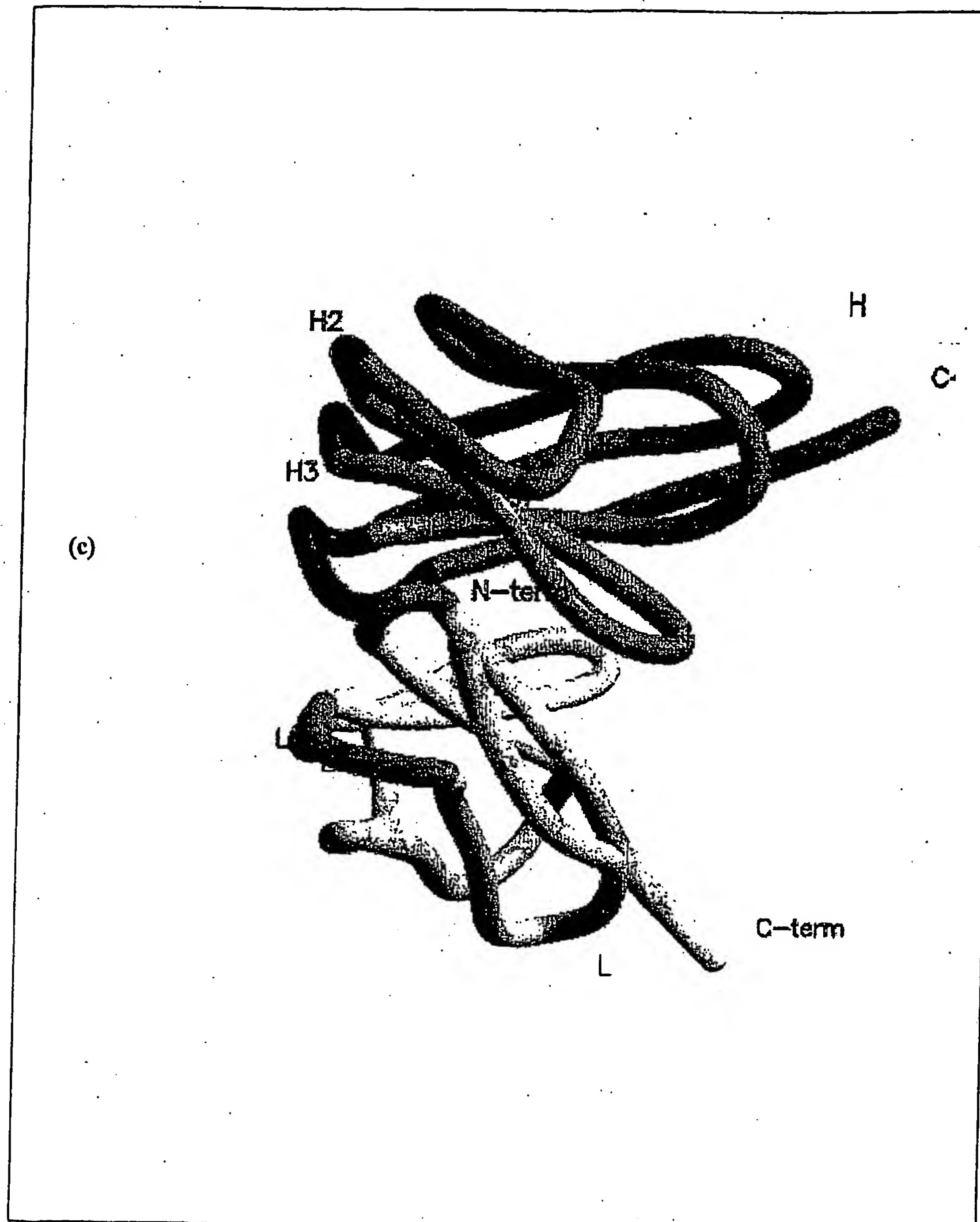


Figure 1(c)

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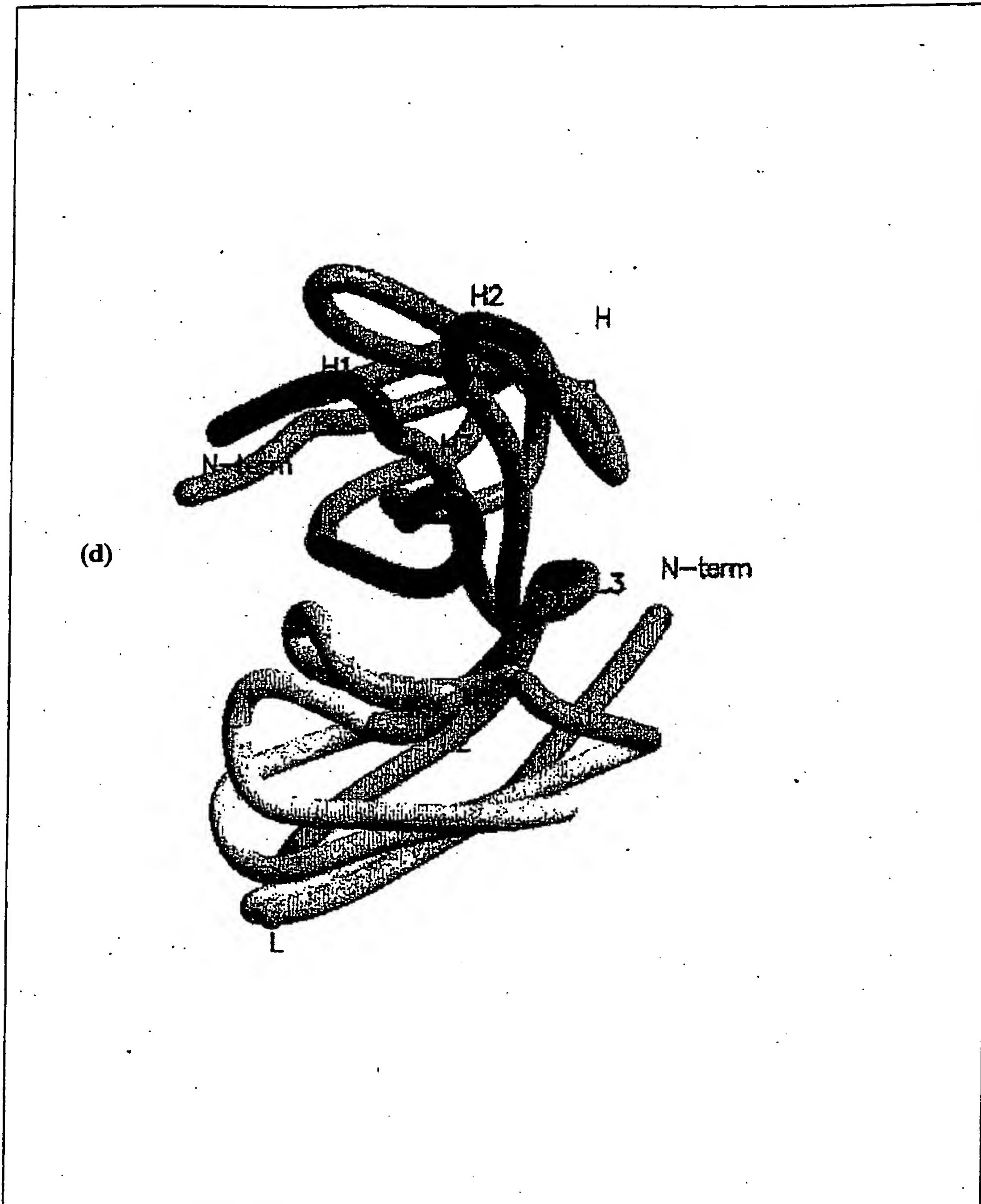
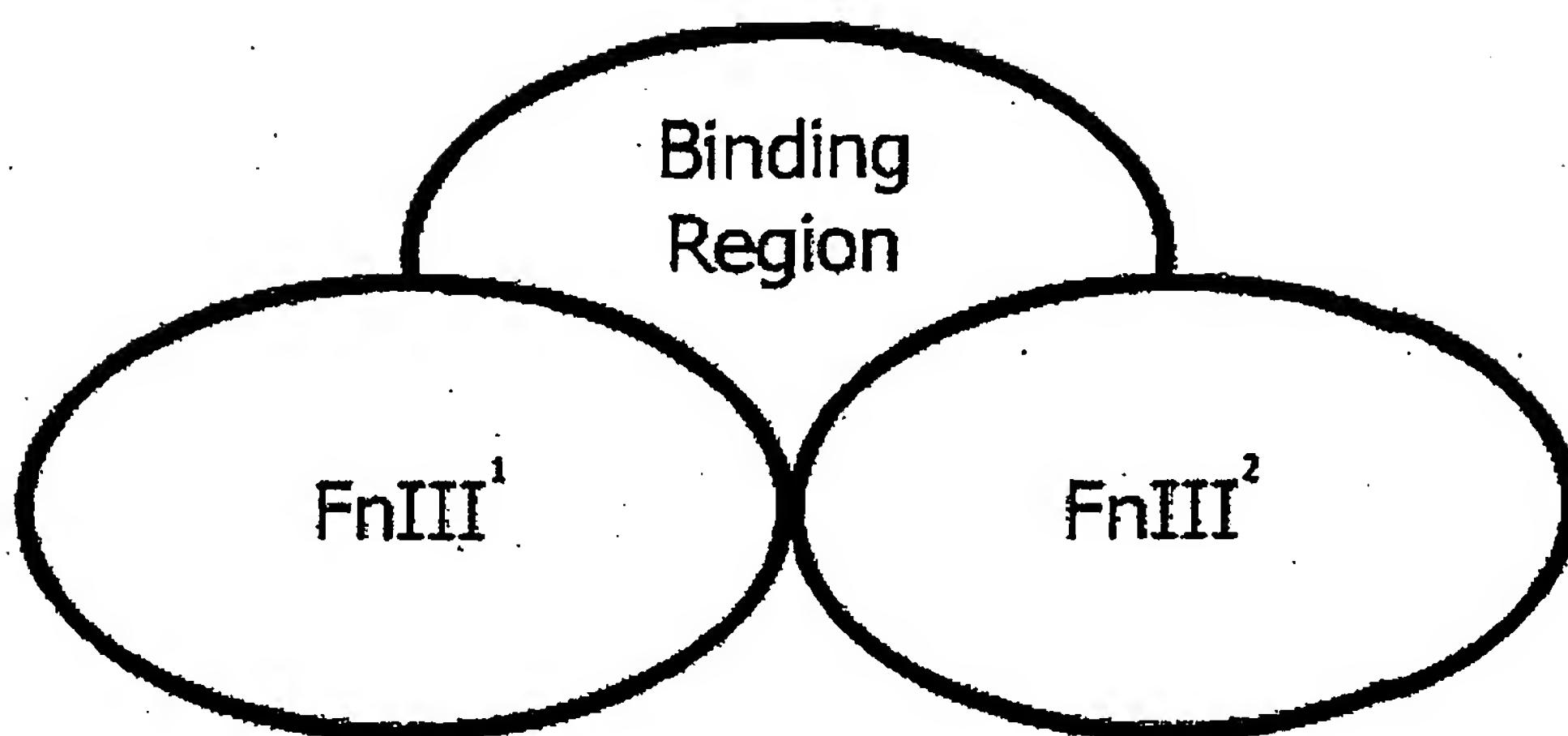


Figure 1(d)

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**Figure 1A**

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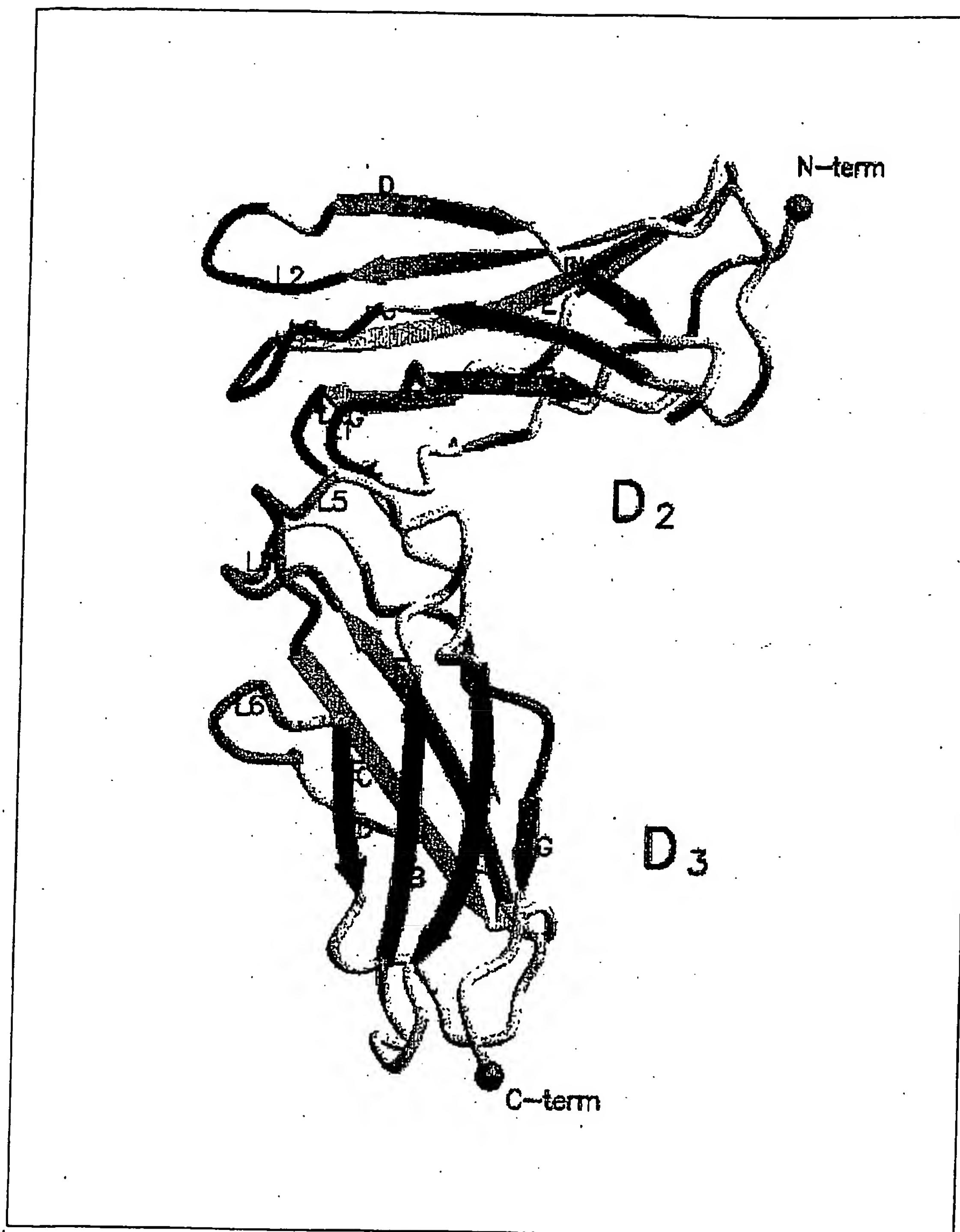


Figure 2(a)

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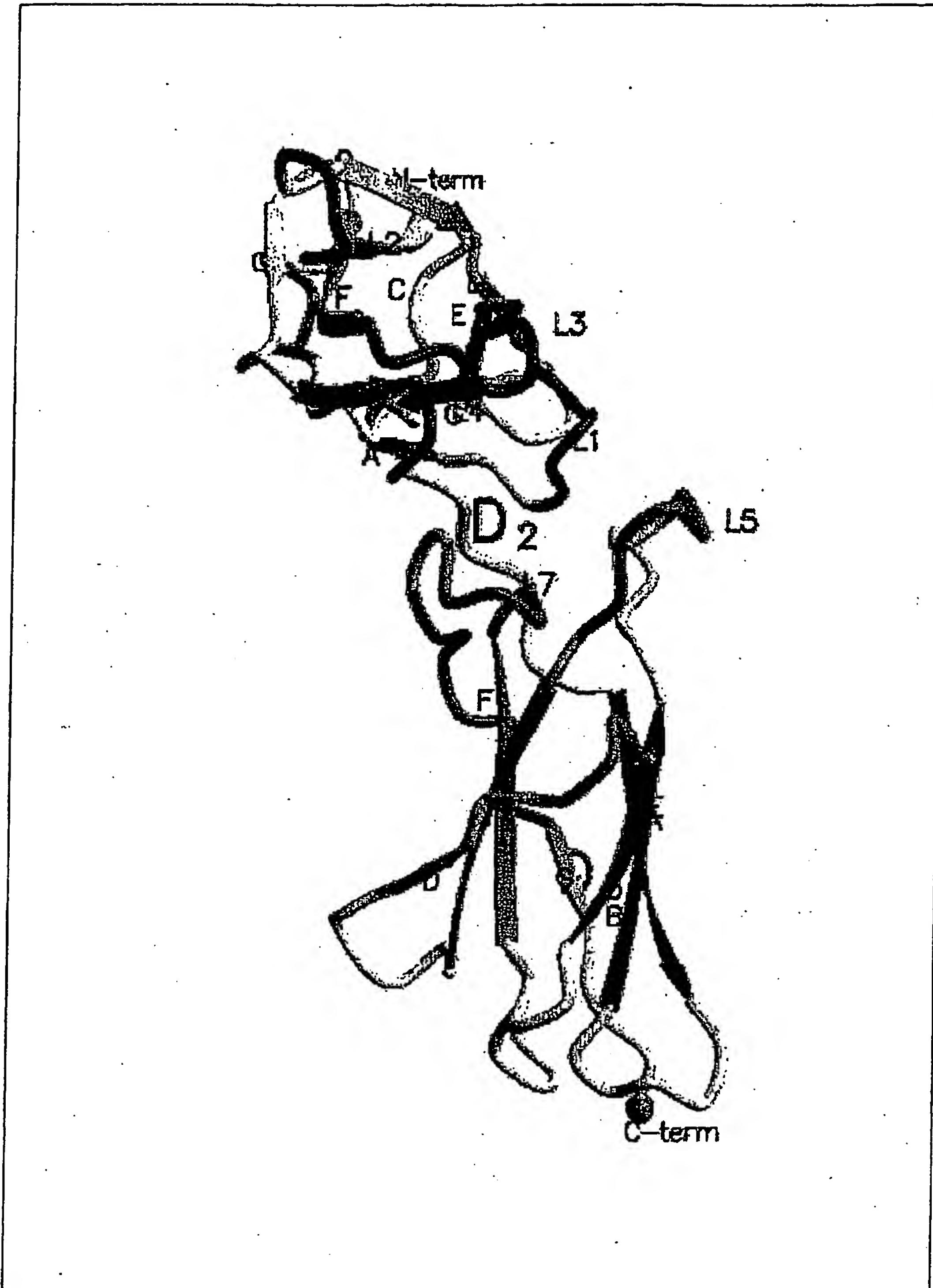


Figure 2(b)

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10 20 30 40 50  
 LAPRRCPAQE VARGVLTSLP GDSVLTCPG VEPEDNATVH WVLRKPAAGS

60 70 80 90 100  
 HPSRWAGMGR RLLLRSVQLH DSGNYSCYRA GRPAGTVHLL VDVPPEEPQLS

A#

110 120 130 140 150  
 CFRKSPLSNV VCEWGPRSTP SLTTKAVLLV RKFQNSPAED FQEPCQYSQE

## B##### C##### D, D'##### A#  
 \*\*\*\*\*

L1

L2

160 170 180 190 200  
 SQKFSCQLAV PEGDSSFYIV SMCVASSVGS KFSKTQTFQG CGILQPDPPA

E##### F##### G##### G'##### A#  
 \*\*\*\*\*

L3

L4

210 220 230 240 250  
 NITVTAVARN PRWLSVTWQD PHSWNSSFYR LRFELRYRAE RSKTFTTWMV

##### B##### C##### D##### A#  
 \*\*\*\*\*

L5

260 270 280 290 300  
 KDLQHHCVIH DAWSGLRHVQ QLRAQEEFGQ GEWSEWSPEA MGTPWTESRS

E##### F##### G#####  
 \*\*\*\*\*

L6

L7

310 320  
 PPAENEVSTP MQALTTNKDD DNIL

# beta sheets; \* loops; ■ first domain (D2); □□□ second domain (D3)

Figure 3

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Approximate positioning of each loop in four of the cytokine receptor family members. The loop positions could vary up to 3 amino acids either side of the box. For example Loop 6 of the prolactin receptor is defined as GQQTEF and not FAQQ as depicted here.

IL6RPRRLRL	-----	VPPEEPQ-LSCFSPNK-ETFVCEWGPRTSPSLTTK
P08887 IL6A_HUMAN	LHDSGNYSCY-RAGRAGTVHLLV	VPPEEPQ-LSCFRKSPLSNVCEWGPRTSPSLTTK
Q14626 I11R_HUMAN	STDEGTYICQTLGALGGTVTLQL	YPPARPV-VSCQAADY-ENFSCTWSPSQISGLPTR
P16471 PRLR_HUMAN	MKENVASATVFTLLLFLNTCLLNG	LPPGKPEIFKCRSPNK-ETFTCWWRPGBTGGLPTN
Q99062 GCSR_HUMAN	-AFLSCCLNWGNQLQILDQVELRA	YPPAIPHNLSCLMNL <b>TSS</b> LICQWEPGPETHLPTS
IL6RPRRLRL	AVLLVHRE-----	GETLMFQEPCQYSQESQKFSCHFGKQYTSMWRTYIVSMSVASS
P08887 IL6A_HUMAN	AVLLVRFKQ-----	SFAEDFQEPCQYSQESQKFSQLA <b>V</b> PEGD-SSFYIVSMCVASS
Q14626 I11R_HUMAN	YLTTSYRKKTVLGADSQRSPSTGPWPCPQD-PLGAARCVVHGAEFW--SQYRINVTEVNP	
P16471 PRLR_HUMAN	YSLTYHRE-----	GETLMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNO
Q99062 GCSR_HUMAN	FTLKSFKSRNC-----	QTQGDSILD <b>C</b> VPK-DGQSHCCIPRKHLLYQNMGIVWVQAENAL
IL6RPRRLRL	VGSKFSDELYVDVTVILQPDPPANITVTAVA-RNPR-----	WLSVTWQDPHLIDLK-TGWFT
P08887 IL6A_HUMAN	VGSKFSKTQTFQGCGILQPDPPANITVTAVA-RNPR-----	WLSVTWQDPHSWNSS-FYR
Q14626 I11R_HUMAN	-LGASTRLLDVSILQSILRPDPPQGLRVESVP-GYPR-----	RLRASWTYPASWPCQ-PHFL
P16471 PRLR_HUMAN	MGSSFSDELYVDVTVIVQPDPPLELAVEVKQ-PEDR-KPYLWIKWSPTL <b>I</b> DLK-TGWFT	
Q99062 GCSR_HUMAN	GTSMSPQTLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAGCLQLCWEPWQPGI <b>H</b> INOKCEL	
IL6RPRRLRL	LRFELRYRAERSKTF <b>T</b> TFW <b>F</b> AG-QQHHSV <b>I</b> HD <b>A</b> WSGLRHVVQLRA <b>K</b> PD-HGYWSEWSPEA	
P08887 IL6A_HUMAN	LRFELRYRAERSKTF <b>T</b> TM <b>V</b> KDLQH <b>H</b> CV <b>I</b> HD <b>A</b> WSGLRHVVQLRA <b>Q</b> EEFG <b>Q</b> GEWSEWSPEA	
Q14626 I11R_HUMAN	L <b>K</b> FR <b>L</b> QYRPAQH <b>P</b> AW <b>S</b> T <b>V</b> E <b>P</b> AG-LEE <b>V</b> ITDAVAGLPHAVRVSARD <b>F</b> LDAGT <b>W</b> ST <b>T</b> WSPEA	
P16471 PRLR_HUMAN	L <b>L</b> YE <b>I</b> RLKPE <b>K</b> AA <b>E</b> WE <b>I</b> H <b>F</b> AG <b>Q</b> -Q <b>T</b> EF <b>K</b> IL <b>S</b> HP <b>G</b> Q <b>K</b> Y <b>L</b> V <b>Q</b> VR <b>C</b> K <b>P</b> D-HGYWSAWSPAT	
Q99062 GCSR_HUMAN	R <b>H</b> KPQR <b>G</b> EA <b>S</b> W <b>A</b> L <b>V</b> GP <b>L</b> PLE <b>A</b> L-Q <b>Y</b> EL <b>C</b> GL <b>L</b> P-ATAY <b>T</b> L <b>Q</b> IRC <b>I</b> R <b>W</b> PL <b>P</b> GH <b>W</b> SD <b>W</b> PSL	
IL6RPRRLRL	MGTPWTE-----	
P08887 IL6A_HUMAN	MGTPWTE RSPPAENEVST-----	PMQALTTN-KDDDNILFRDSANATSLPVQ
Q14626 I11R_HUMAN	WGTPSTG IPKEIPAWGQL-----	HTQPEVEP-QVDSAPP <i>PRPSLQPHPRLLD</i>
P16471 PRLR_HUMAN	FIQIPSD TMNDTTVWISAVAVICLIIIVWAVALKGYSMVT <b>C</b> IFPPVPGPKIKGFD <b>A</b> H	
Q99062 GCSR_HUMAN	ELRTTER PTVRLDTWWRQR-QLDPRTVQLFWKPVPLEEDSGRIQGYVVS-WRPSGQAGA	

Figure 3A

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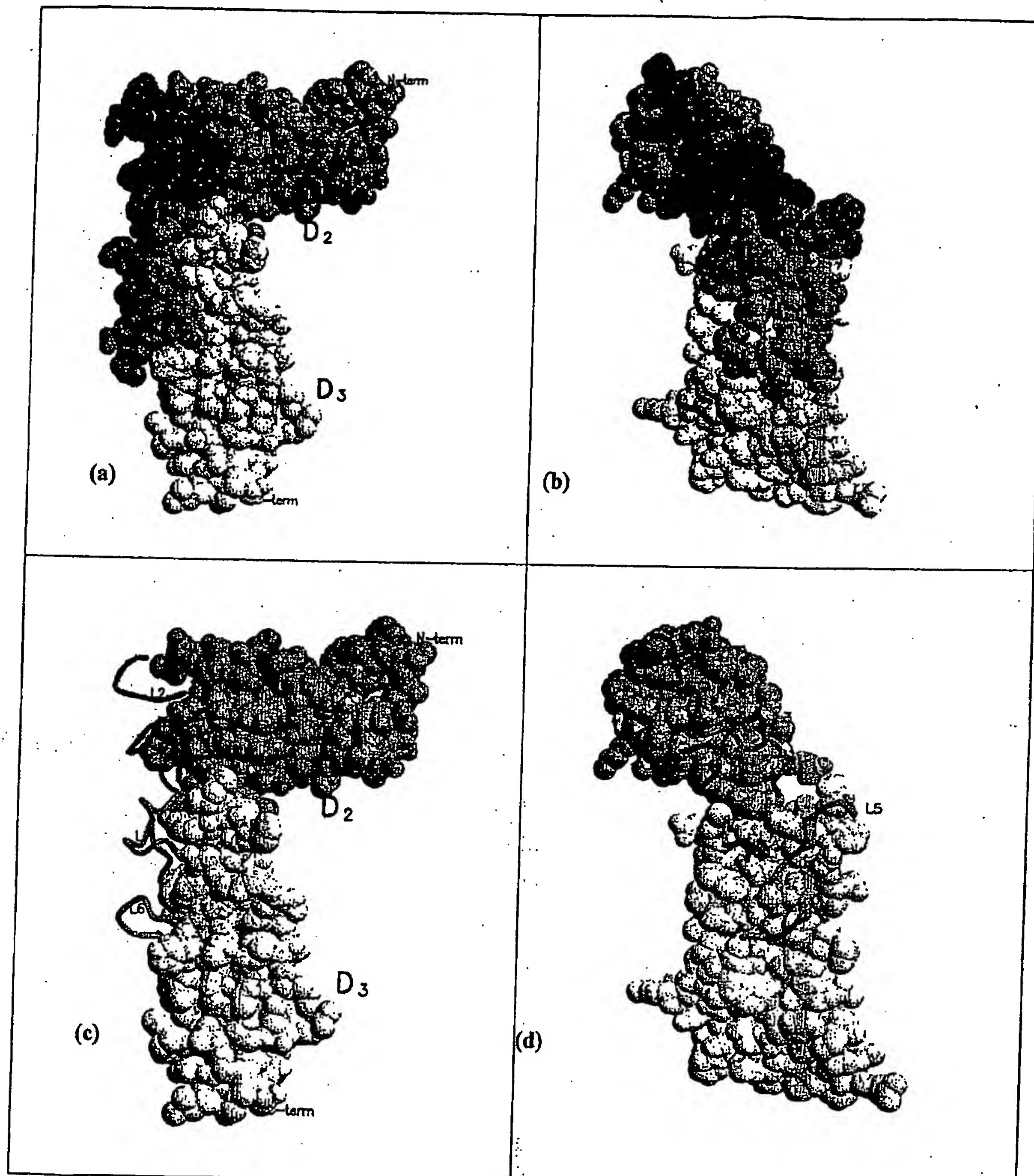


Figure 4

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hGCSF_122-334	YDIAH	SM	SCAHL	YDIAHSCAHL
hGCSF_121-333	YDIAH	SM	SCAHL	YDIAHSCAHL
hcommBR_26-240	ETIB	QT	RCNDY	ETIBRCNDY
hcommBR_30-243	ETV	HTP	QCHNDY	ETVQCHNDY
hIL3BR_30-244	ETV	HTP	EGNDY	ETVEGNDY
baommBR_240-439	EDAOQ	ON	EGNDY	EDAOQEGNDY
mcommBR_243-442	EDAOQ	ON	EGNDY	EDAOQEGNDY
hIL6BR_244-441	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hgp130_124-325	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hgp130_124-323	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hGHR_46-262	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hH_GHR_46-271	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hIL12p40_122-328	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hIL12p40_118-332	EDKAQHOM	QCHFD	EGNDY	EDKAQHOMEGNDY
hEPOR_39-247	AAFLYR	EN	LCNTOR	AAFLYRLCNTOR
hEPOR_39-246	AAFLYR	EN	LCNTOR	AAFLYRLCNTOR
hIL6R_112-317	VEPEH	O	SCERES	VEPEHSCERES
hIL6R_108-313	VEPEH	O	SCERES	VEPEHSCERES
hIL4R_24-224	UNMKQEN	TCHSDY	SCERES	UNMKQENSCERES
hIL4R_24-225	SIKQEN	TCHSDY	SCERES	SIKQENSCERES
hPRLR_24-229	COLTQEN	EP	SCERES	COLTQENSCERES
hPRLR_19-224	EDSBRK	R	SCERES	EDSBRKSCERES
hCRLF1_133-342	LEPKR	VNS	SCERES	LEPKRSCERES
hCRLF1_136-345	LEPSK	VNS	SCERES	LEPSKSCERES
hIL12B2R_122-320	VEPEH	ON	SCERES	VEPEHSCERES
hIL12B2R_135-336	VEPEH	ON	SCERES	VEPEHSCERES
hIL11R_111-318	YDIAH	V	SCQAVD	YDIAHSCQAVD
hIL11RA1_111-318	FEAR	E	SCQAVD	FEARSCQAVD
hIL11RA2_111-318	FEAR	E	SCQAVD	FEARSCQAVD
hCNTR_107-317	LEPKE	V	SCRSNT	LEPKESCRSNT
hCNTR_107-317	LEPKE	V	SCRSNT	LEPKESCRSNT
hCR_23-229	MLAATYR	R	SCRSNT	MLAATYRSCRSNT
hCR_23-228	MLAATYR	R	SCRSNT	MLAATYRSCRSNT
hthromboR_27-285	AVVNSQDSE	R	SCRSNT	AVVNSQDSESCRSNT
hthromboR_27-277	DSVNSQDSE	R	SCRSNT	DSVNSQDSESCRSNT
hleptinR_429-638	DENIN	SCETDS	SCRSNT	DENINSCRSNT
hleptinR_427-636	DENIN	SCETDS	SCRSNT	DENINSCRSNT
hleptinR_124-332	DENIN	SCETDS	SCRSNT	DENINSCRSNT
hleptinR_124-330	DENIN	SCETDS	SCRSNT	DENINSCRSNT
hIL21R_17-229	ENW	ED	EDCMK	ENWEDCMK
hIL21R_17-229	ENW	ED	EDCMK	ENWEDCMK
hthromboR_285-490	ENW	ED	EDCMK	ENWEDCMK
hthromboR_277-481	ENW	ED	EDCMK	ENWEDCMK
hwsk1_34-232	ESR	Q	EDCMK	ESREDCMK
hwsk1_29-226	ESR	Q	EDCMK	ESREDCMK
hIL2BR_30-235	ENW	ED	EDCMK	ENWEDCMK
hIL2BR_30-236	ENW	ED	EDCMK	ENWEDCMK
hIL9R_48-261	ENW	ED	EDCMK	ENWEDCMK
hIL9R_47-261	ENW	ED	EDCMK	ENWEDCMK
hIL12B1R_42-234	ENW	ED	EDCMK	ENWEDCMK
hIL12B1R_43-256	ENW	ED	EDCMK	ENWEDCMK
hIL13AIR_123-337	EDEEETR	Q	EDCMK	EDEEETRQEDCMK
hIL13AIR_121-333	EDEEETR	Q	EDCMK	EDEEETRQEDCMK
hIL13A2R_134-333	EDEEETR	Q	EDCMK	EDEEETRQEDCMK
hIL13A2R_128-327	EDEEETR	Q	EDCMK	EDEEETRQEDCMK
hILSR_123-332	EDSNTSUN	T	EDCMK	EDSNTSUNEDCMK
hILSR_120-329	EDSNTSUN	T	EDCMK	EDSNTSUNEDCMK
hGMCSPR_115-348	EDSNTSUN	T	EDCMK	EDSNTSUNEDCMK
hGMCSPR_124-352	EDSNTSUN	T	EDCMK	EDSNTSUNEDCMK
hIL3R_100-293	EDT	ED	EDCMK	EDTEDCMK
hIL3R_113-322	EDT	ED	EDCMK	EDTEDCMK
hcommGR_39-253	EDT	ED	EDCMK	EDTEDCMK
hcommGR_39-254	EDT	ED	EDCMK	EDTEDCMK
hTSLPR_30-216	EDT	ED	EDCMK	EDTEDCMK
hTSLPR_27-217	EDT	ED	EDCMK	EDTEDCMK
hLIFR_48-246	EDT	ED	EDCMK	EDTEDCMK
hLIFR_47-241	EDT	ED	EDCMK	EDTEDCMK
hLIFR_391-534	EDT	ED	EDCMK	EDTEDCMK
hLIFR_326-529	EDT	ED	EDCMK	EDTEDCMK
hOSMR_28-140	EDT	ED	EDCMK	EDTEDCMK
hOSMR_25-139	EDT	ED	EDCMK	EDTEDCMK
hOSMR_238-429	EDT	ED	EDCMK	EDTEDCMK
hOSMR_232-426	EDT	ED	EDCMK	EDTEDCMK
hIL7R_28-236	EDT	ED	EDCMK	EDTEDCMK
hIL7R_28-236	EDT	ED	EDCMK	EDTEDCMK
domecyt1_115-330	EDT	ED	EDCMK	EDTEDCMK
domecyt2_176-391	EDT	ED	EDCMK	EDTEDCMK
consensus	EDT	ED	EDCMK	EDTEDCMK
hGMR	EDT	ED	EDCMK	EDTEDCMK
oGMR	EDT	ED	EDCMK	EDTEDCMK
mChirica_cedric	EDT	ED	EDCMK	EDTEDCMK
hCirica	EDT	ED	EDCMK	EDTEDCMK
ruler 1, . . . , 10, . . . , 20, . . . , 30, . . . , 40, . . . , 50	EDT	ED	EDCMK	EDTEDCMK

Figure 5A

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60.....70.....80.....90.....100.....110.....120

**Figure 5A (cont)**

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**Figure 5A (cont)**

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Figure 5B

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**Figure 5B (cont)**

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**Figure 5B (cont)**

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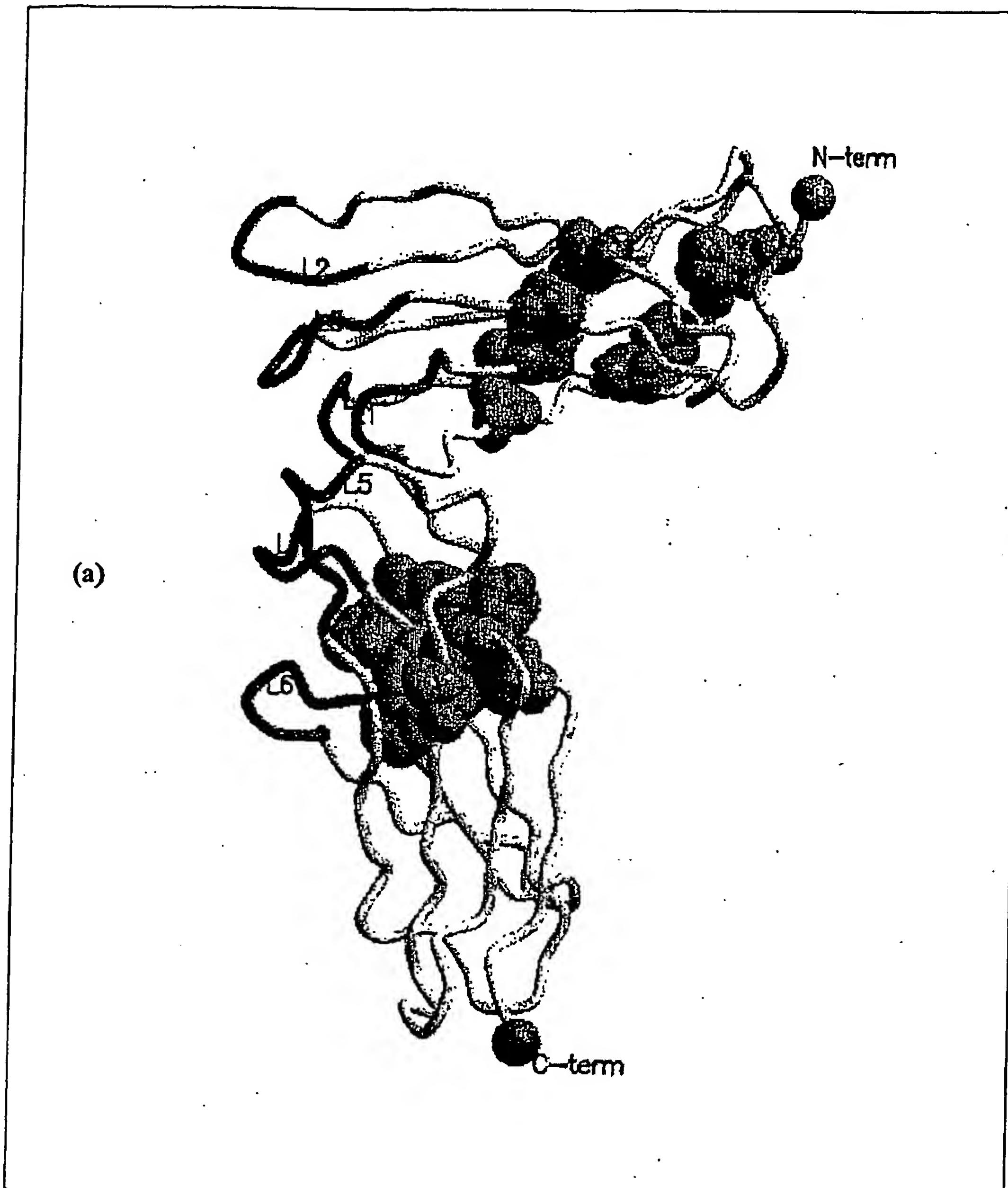


Figure 6(a)

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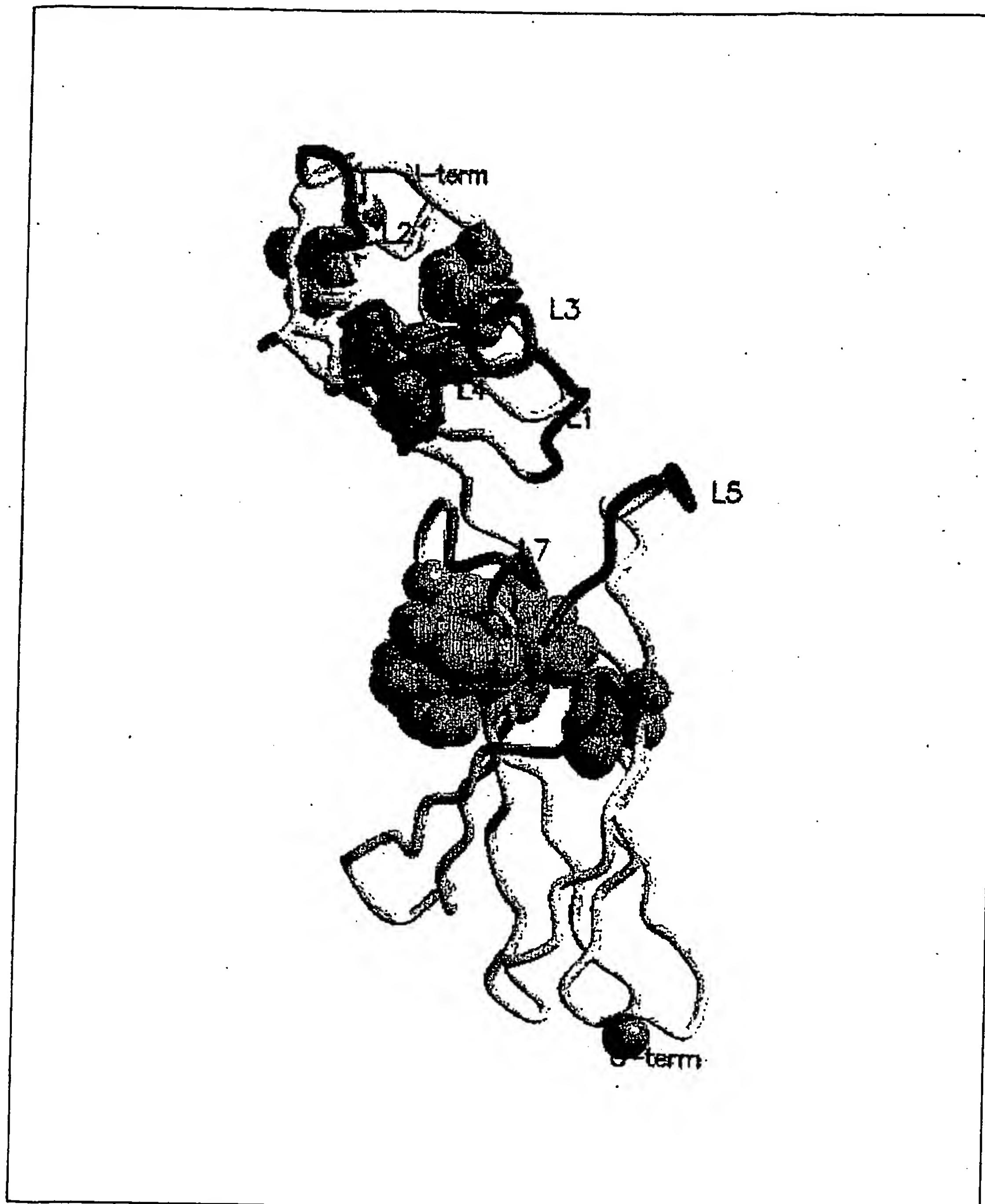


Figure 6(b)

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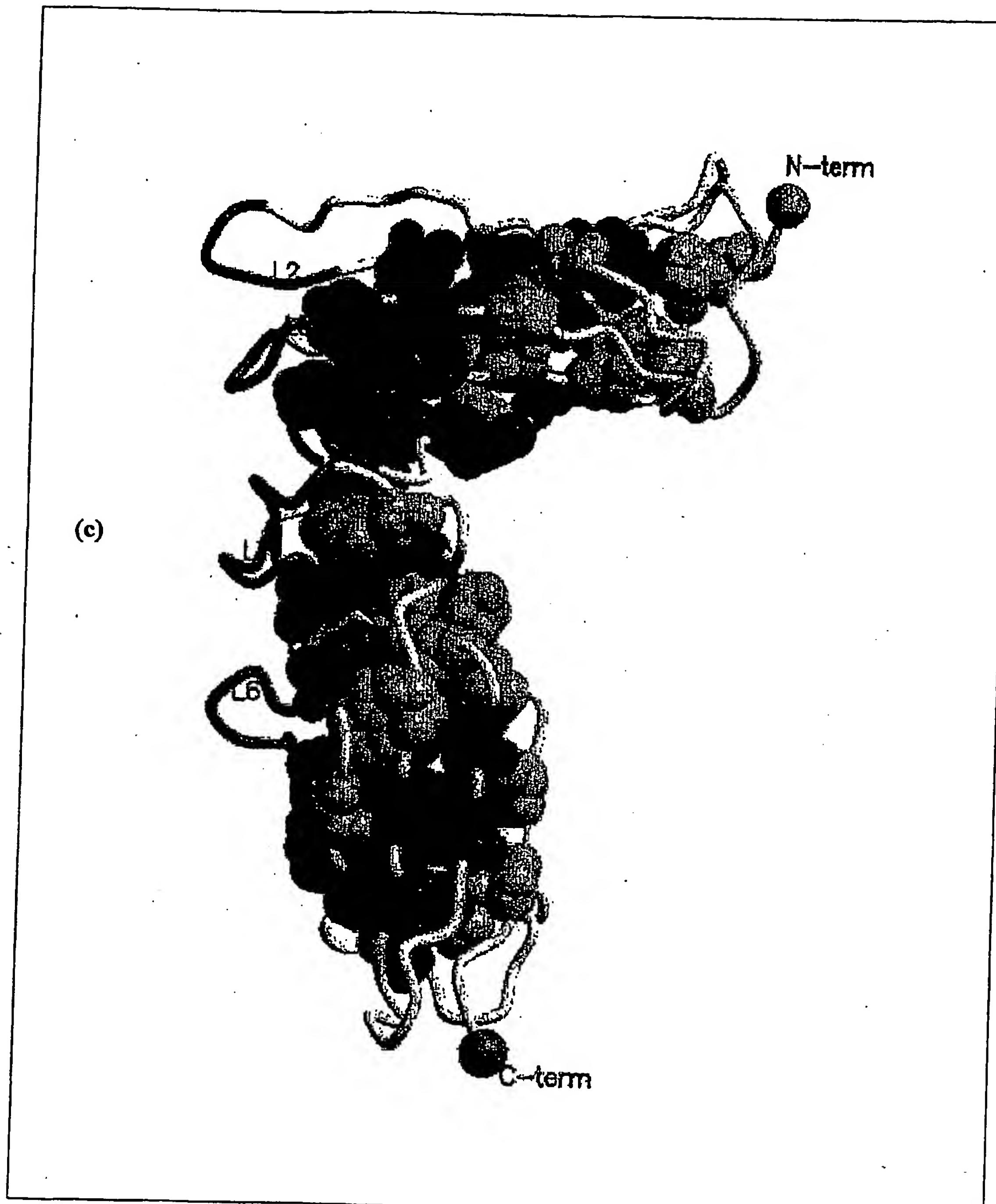


Figure 6(c)

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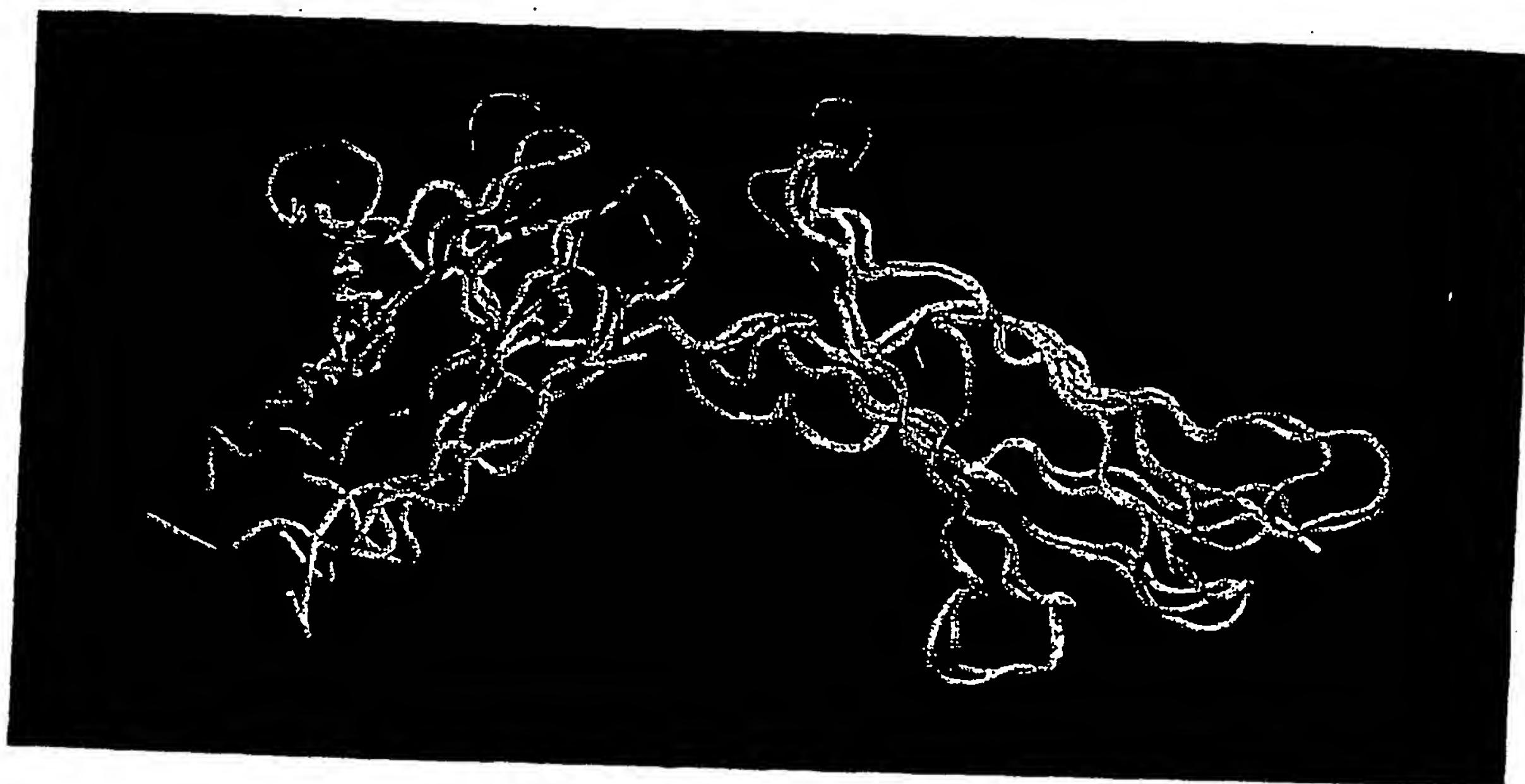
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Figure 6(d)

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**Figure 7**

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